

CLAIM AMENDMENTS

1. (Currently Amended) An allelic ladder mixture comprising one or more of the following allelic ladders :-

i) an allelic ladder for locus HUMVWFA31/A comprising one or more alleles

with a short tandem repeat sequence consisting of sequences :-

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1; or

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2; or

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3;

ii) an allelic ladder for locus HUMTHO1 comprising an allele with a short

tandem repeat sequence consisting of sequence :-

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

iii) an allelic ladder for locus D8S1179 comprising an allele with a short tandem

repeat sequence consisting of sequence:-

(TCTA)₂ TCTG(TCTA)₁₆ - SEQ ID NO 6;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more alleles

with a short tandem repeat sequence consisting of sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID

NO 7; or

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 8; or

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 9; or

(TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 10; or

(TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 11; or

(TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 12; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 13; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 14; or

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 15; or

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 16; or

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 17; or

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 18;

v) an allelic ladder for locus D21S11 comprising one or more alleles with a short

tandem repeat sequence consisting of sequences :-

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA

(TCTA)₆ TCGTCT - SEQ ID NO 19; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 20 or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 21; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₈ TCGTCT - SEQ ID NO 22; or

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₉ TCGTCT - SEQ ID NO 23; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₀ TCGTCT - SEQ ID NO 24; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 25; or

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 26; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 27; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TA TCTA TCGTCT - SEQ ID NO 28; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TA TCTA TCGTCT - SEQ ID NO 29; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TA TCTA TCGTCT - SEQ ID NO 30; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₄ TATCTA TCGTCT - SEQ ID NO 31; or

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 32; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 33; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TCGTCT - SEQ ID NO 34; or

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 35;

vi) an allelic ladder for locus D18S51 comprising an allele with a short tandem repeat sequence consisting of sequence:-

(AGAA)₈ - SEQ ID NO 36.

2. (Original) An allelic ladder mixture according to claim 1 in which the mixture includes allelic ladders for a plurality of loci selected from HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.

3. (Original) An allelic ladder mixture according to claim 1 the mixture including allelic ladders for at least four loci.

4. (Cancelled)

5. (Previously Presented) An allelic ladder mixture according to claim 1 in which the allelic ladders in the mixture each include at least 7 alleles.

6. (Original) An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 9 alleles; the HUMTHO1 allelic ladder includes at least 7; the D8S1179 allelic ladder includes at least 9 alleles; the HUMFIBRA/FGA allelic ladder includes at least 18 alleles or is present as HUMFIBRA/FGA/LW and HUMFIBRA/FGA/HW with the HUMFIBRA/FGA/LW ladder including at least 16 alleles, the HUMFIBRA/FGA/HW ladder including at least 6 alleles; the D21S11 allelic ladder includes at least 14 alleles; and the D18S51 ladder includes at least 15 alleles.

7. (Original) An allelic ladder mixture according to claim 1 in which one or more of the allelic ladders in the mixture comprises at least 4 pairs of alleles 4 base pairs from each other.

8. (Original) An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 7 pairs of alleles 4 base pairs from each other; the HUMTHO1 allelic ladder includes at least 5 pairs of alleles 4 base pairs from each other; the D8S1179 allelic ladder includes at least 8 pairs of alleles 4 base pairs from each other; the HUMFIBRA/FGA allelic ladder includes at least 17 pairs of alleles 4 base pairs from each other; the D21S11 allelic ladder includes at least 3 pairs of alleles 4 base pairs from each other; and the D18S51 ladder includes at least 13 pairs of alleles 4 base pairs from each other.

9. (Original) An allelic ladder mixture according to claim 8 in which the D21S11 allelic ladder includes at least 8 pairs of alleles 8 base pairs from each other.

10. (Original) An allelic ladder mixture according to claim 1 in which the ladders, if present, are provided such that the HUMVWFA31/A ladder includes alleles ranging from 130 base pairs upwards and/or from 166 base pairs downwards; the HUMTHO1 ladder includes alleles ranging from 150 base pairs upwards and/or 189 base pairs downwards; the D8S1179 ladder includes alleles ranging from 157 base pairs upwards and/or 201 base pairs downwards; the HUMFIBRA/FGA ladder includes alleles ranging from 173 base pairs upwards and/or 298 base pairs downwards; the D21S11 ladder includes alleles ranging from 203 base pairs upwards and/or 255 base pairs downwards; and the D18S51 ladder includes alleles ranging from 270 base pairs upwards and/or 326 downwards.

11. (Currently Amended) An allelic ladder mixture comprising an allelic ladder for one or more of the following loci, with lowest and highest allele designation ~~molecular weight allele and uppermost molecular weight allele designation~~ as follows :-

	Locus	<u>Low MW allele</u> <u>Lowest</u> <u>Designation</u>	<u>High MW allele</u> <u>Highest</u> <u>Designation</u>
a)	HUMVWFA31/A	10	21
b)	HUMTH01	4	13.3
c)	D8S1179	7	19
d)	HUMFIBRA/FGA	16.1	50.2
e)	D21S11	53	81
f)	D18S51	8	27

12. (Cancelled)

13. (Original) An allelic ladder mixture according to claim 11 in which the mixture includes allelic ladders for loci HUMVWFA31/A, HUMTH01, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.

14. (Currently Amended) A method of analysing one or more samples comprising:

- a) obtaining genomic DNA from the sample;
- b) amplifying the DNA;
- c) obtaining an indication of one or more of the constituent parts of the sample;

and comparing the indications with an allelic ladder mixture comprising one or more of the following allelic ladders :-

- i) an allelic ladder for locus HUMVWFA31/A comprising one or more alleles with a short tandem repeat sequence consisting of sequences :-

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1; or

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2; or

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3

- ii) an allelic ladder for locus HUMTHO1 comprising an allele with a short tandem repeat sequence consisting of sequence :-

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

- iii) an allelic ladder for locus D8S1179 comprising an allele with a short tandem repeat sequence consisting of sequence:-

(TCTA)₂ TCTG (TCTA)₁₆ - SEQ ID NO 6;

- iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more alleles with a short tandem repeat sequence consisting of the sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID

NO 7; or

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 8; or

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 9; or

(TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 10; or

(TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 11; or

(TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 12; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 13; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 14; or

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 15; or

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 16; or

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 17; or

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 18;

v) an allelic ladder for locus D21S11 comprising one or more alleles

with a short tandem repeat sequence consisting of sequences :-

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₆ TCGTCT - SEQ ID NO 19; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 20; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 21; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₈ TCGTCT - SEQ ID NO 22; or

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₉ TCGTCT - SEQ ID NO 23; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₀ TCGTCT - SEQ ID NO 24; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 25; or

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 26; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 27; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TA TCTA TCGTCT - SEQ ID NO 28; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TA TCTA TCGTCT - SEQ ID NO 29; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TA TCTA TCGTCT - SEQ ID NO 30; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₄ TATCTA TCGTCT - SEQ ID NO 31; or

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 32; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 33; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TCGTCT - SEQ ID NO 34; or

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 35;

vi) an allelic ladder for locus D18S51 comprising an allele with a short tandem repeat sequence consisting of sequence :-

(AGAA)₈ - SEQ ID NO 36.

15. (Previously Presented) A method according to claim 14 in which the DNA sample is one or more of a sample taken from the scene of a crime, a sample associated with the scene of a crime, a sample obtained from a suspect, a sample obtained from a human under consideration or a reference sample.

16. (Original) A method according to claim 14 in which the sample is amplified using a polymerase chain reaction and primers for one or more of loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 or D18S51 are employed.

17. (Currently Amended) One or more isolated alleles with a short tandem repeat sequence consisting of sequences:

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1;

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2;

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3;

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

(TCTA)₂ TCTG (TCTA)₁₆ - SEQ ID NO 6;

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID NO 7;

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 8;

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 9;

(TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 10;

(TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 11;

(TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 12;

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 13;

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 14;

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 15;

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC
(TTCC)₄ - SEQ ID NO 16;

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃ CTCC
(TTCC)₄ - SEQ ID NO 17;

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃ CTCC
(TTCC)₄ - SEQ ID NO 18;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₆
TCGTCT - SEQ ID NO 19;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉ TCGTCT - SEQ
ID NO 20;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀ TCGTCT - SEQ
ID NO 21;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₈
TCGTCT - SEQ ID NO 22;

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 23;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 24;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁
TCGTCT - SEQ ID NO 25;

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁
TCGTCT - SEQ ID NO 26;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 27;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁ TA
TCTA TCGTCT - SEQ ID NO 28;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂ TA
TCTA TCGTCT - SEQ ID NO 29;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₃ TA
TCTA TCGTCT - SEQ ID NO 30;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₄
TATCTA TCGTCT - SEQ ID NO 31;

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 32;

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 33;

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₃
TCGTCT - SEQ ID NO 34;

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 35; or

(AGAA)₈ - SEQ ID NO 36.

18. (Previously Presented) One or more alleles according to claim 17 in which the alleles are provided purified from alleles other than those of HUMVWFA31/A, HUMTH01, D8S1179, HUMFIBRA/FGA, D21S11, D18S51 or AMG loci.

19-22. (Cancelled)

23. (New) An allelic ladder mixture comprising one or more of the following allelic ladders :-

i) an allelic ladder for locus HUMVWFA31/A comprising one or more alleles having a flanking sequence on either side of a sequence consisting of sequences :-

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1; or

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2; or

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3;

ii) an allelic ladder for locus HUMTHO1 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence :-

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

iii) an allelic ladder for locus D8S1179 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence:-

(TCTA)₂ TCTG(TCTA)₁₆ - SEQ ID NO 6;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more alleles having a flanking sequence on either side of a sequence consisting of sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID

NO 7; or

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 8; or

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ

ID NO 9; or

(TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 10; or

(TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 11; or

(TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ

ID NO 12; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 13; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 14; or

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 15; or

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 16; or

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 17; or

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃

CTCC (TTCC)₄ - SEQ ID NO 18;

v) an allelic ladder for locus D21S11 comprising one or more alleles having a flanking sequence on either side of a sequence consisting of sequences :-

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA

(TCTA)₆ TCGTCT - SEQ ID NO 19; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 20 or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 21; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₈ TCGTCT - SEQ ID NO 22; or

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₉ TCGTCT - SEQ ID NO 23; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₀ TCGTCT - SEQ ID NO 24; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 25; or

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 26; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 27; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TA TCTA TCGTCT - SEQ ID NO 28; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TA TCTA TCGTCT - SEQ ID NO 29; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TA TCTA TCGTCT - SEQ ID NO 30; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₄ TATCTA TCGTCT - SEQ ID NO 31; or

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 32; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 33; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TCGTCT - SEQ ID NO 34; or

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 35;

vi) an allelic ladder for locus D18S51 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence:-

(AGAA)₈ - SEQ ID NO 36.

24. (New) An allelic ladder mixture according to claim 23 in which the mixture includes allelic ladders for a plurality of loci selected from HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.

25. (New) An allelic ladder mixture according to claim 23 the mixture including allelic ladders for at least four loci.

26. (New) An allelic ladder mixture according to claim 23 in which the allelic ladders in the mixture each include at least 7 alleles.

27. (New) An allelic ladder mixture according to claim 23 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 9 alleles; the HUMTHO1 allelic ladder includes at least 7; the D8S1179 allelic ladder includes at least 9 alleles; the HUMFIBRA/FGA allelic ladder includes at least 18 alleles or is present as HUMFIBRA/FGA/LW and HUMFIBRA/FGA/HW with the HUMFIBRA/FGA/LW ladder including at least 16 alleles, the HUMFIBRA/FGA/HW ladder including at least 6 alleles; the D21S11 allelic ladder includes at least 14 alleles; and the D18S51 ladder includes at least 15 alleles.

28. (New) An allelic ladder mixture according to claim 23 in which one or more of the allelic ladders in the mixture comprises at least 4 pairs of alleles 4 base pairs from each other.

29. (New) An allelic ladder mixture according to claim 23 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 7 pairs of alleles 4 base pairs from each other; the HUMTHO1 allelic ladder includes at least 5 pairs of alleles 4 base pairs from each other; the D8S1179 allelic ladder includes at least 8 pairs of alleles 4 base pairs from each other; the HUMFIBRA/FGA allelic ladder includes at least 17 pairs of alleles 4 base pairs from each other; the D21S11 allelic ladder includes at least 3 pairs of alleles 4 base pairs from each other; and the D18S51 ladder includes at least 13 pairs of alleles 4 base pairs from each other.

30. (New) An allelic ladder mixture according to claim 29 in which the D21S11 allelic ladder includes at least 8 pairs of alleles 8 base pairs from each other.

31. (New) An allelic ladder mixture according to claim 23 in which the ladders, if present, are provided such that the HUMVWFA31/A ladder includes alleles ranging from 130 base pairs upwards and/or from 166 base pairs downwards; the HUMTHO1 ladder includes alleles ranging from 150 base pairs upwards and/or 189 base pairs downwards; the D8S1179 ladder includes alleles ranging from 157 base pairs upwards and/or 201 base pairs downwards; the HUMFIBRA/FGA ladder includes alleles ranging from 173 base pairs upwards and/or 298 base pairs downwards; the D21S11 ladder includes alleles ranging from 203 base pairs upwards and/or 255 base pairs downwards; and the D18S51 ladder includes alleles ranging from 270 base pairs upwards and/or 326 downwards.

32. (New) A method of analysing one or more samples comprising:

- a) obtaining genomic DNA from the sample;
- b) amplifying the DNA;
- c) obtaining an indication of one or more of the constituent parts of the sample;

and comparing the indications with an allelic ladder mixture comprising one or more of the following allelic ladders :-

- i) an allelic ladder for locus HUMVWFA31/A comprising one or more alleles having a flanking sequence on either side of a sequence consisting of sequences :-

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1; or

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2; or

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3

ii) an allelic ladder for locus HUMTHO1 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence :-

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

iii) an allelic ladder for locus D8S1179 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence:-

(TCTA)₂ TCTG (TCTA)₁₆ - SEQ ID NO 6;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more alleles having a flanking sequence on either side of a sequence consisting of the sequences :-

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID NO 7; or

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 8; or

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 9; or

(TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 10; or

(TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 11; or

(TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 12; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 13; or

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃
CTCC (TTCC)₄ - SEQ ID NO 14; or

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃
CTCC (TTCC)₄ - SEQ ID NO 15; or

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃
CTCC (TTCC)₄ - SEQ ID NO 16; or

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃
CTCC (TTCC)₄ - SEQ ID NO 17; or

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃
CTCC (TTCC)₄ - SEQ ID NO 18;

v) an allelic ladder for locus D21S11 comprising one or more alleles
having a flanking sequence on either side of a sequence consisting of sequences :-

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₆ TCGTCT - SEQ ID NO 19; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 20; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 21; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₈ TCGTCT - SEQ ID NO 22; or

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₉ TCGTCT - SEQ ID NO 23; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₀ TCGTCT - SEQ ID NO 24; or

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 25; or

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TCGTCT - SEQ ID NO 26; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 27; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₁ TA TCTA TCGTCT - SEQ ID NO 28; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TA TCTA TCGTCT - SEQ ID NO 29; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TA TCTA TCGTCT - SEQ ID NO 30; or

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₄ TATCTA TCGTCT - SEQ ID NO 31; or

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 32; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 33; or

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₃ TCGTCT - SEQ ID NO 34; or

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA
(TCTA)₁₂ TCGTCT - SEQ ID NO 35;

vi) an allelic ladder for locus D18S51 comprising an allele having a flanking sequence on either side of a sequence consisting of sequence :-
(AGAA)₈ - SEQ ID NO 36.

33. (New) A method according to claim 32 in which the DNA sample is one or more of a sample taken from the scene of a crime, a sample associated with the scene of a crime, a sample obtained from a suspect, a sample obtained from a human under consideration or a reference sample.

34. (New) A method according to claim 32 in which the sample is amplified using a polymerase chain reaction and primers for one or more of loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 or D18S51 are employed.

35. (New) One or more isolated alleles having a flanking sequence on either side of a sequence consisting of sequences:

TCTA TCTG TCTA (TCTG)₄ (TCTA)₃ - SEQ ID NO 1;

TCTA (TCTG)₄ (TCTA)₇ - SEQ ID NO 2;

(TCTA)₂ (TCTG)₄ (TCTA)₃ TCCA (TCTA)₃ - SEQ ID NO 3;

(TCAT)₄ CAT (TCAT)₇ TCGT TCAT - SEQ ID NO 4;

(TCTA)₂ TCTG (TCTA)₁₆ - SEQ ID NO 6;

(TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₃ CTCC (TTCC)₂ - SEQ ID NO 7;

(TTTC)₃ TTTT TTCT (CTTT)₁₃ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 8;

(TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂ - SEQ ID NO 9;
 (TTTC)₄ TTTT TT (CTTT)₁₅ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 10;
 (TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 11;
 (TTTC)₄ TTTT TT (CTTT)₁₇ (CTTC)₃ (CTTT)₃ CTCC (TTCC)₄ - SEQ ID NO 12;
 (TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₄ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 13;

(TTTC)₄ TTTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 14;

(TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₃ (CTTT)₁₄ (CTTC)₃ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 15;

(TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 16;

(TTTC)₄ TTTT TT (CTTT)₁₂ (CTGT)₅ (CTTT)₁₄ (CTTC)₃ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 17;

(TTTC)₄ TTTT TT (CTTT)₁₄ (CTGT)₃ (CTTT)₁₄ (CTTC)₄ (CTTT)₃ CTCC
 (TTCC)₄ - SEQ ID NO 18;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA(TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₆
 TCGTCT - SEQ ID NO 19;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉ TCGTCT - SEQ
 ID NO 20;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀ TCGTCT - SEQ
 ID NO 21;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₈
TCGTCT - SEQ ID NO 22;

(TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₉
TCGTCT - SEQ ID NO 23;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀
TCGTCT - SEQ ID NO 24;

(TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁
TCGTCT - SEQ ID NO 25;

(TCTA)₆ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁
TCGTCT - SEQ ID NO 26;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 27;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₁ TA
TCTA TCGTCT - SEQ ID NO 28;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂ TA
TCTA TCGTCT - SEQ ID NO 29;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₃ TA
TCTA TCGTCT - SEQ ID NO 30;

(TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₄
TATCTA TCGTCT - SEQ ID NO 31;

(TCTA)₁₀ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂
TCGTCT - SEQ ID NO 32;

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂

TCGTCT - SEQ ID NO 33;

(TCTA)₁₁ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₃

TCGTCT - SEQ ID NO 34;

(TCTA)₁₃ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₂

TCGTCT - SEQ ID NO 35; or

(AGAA)₈ - SEQ ID NO 36.

36. (New) One or more alleles according to claim 35 in which the alleles are provided purified from alleles other than those of HUMVWFA31/A, HUMTH01, D8S1179, HUMFIBRA/FGA, D21S11, D18S51 or AMG loci.